CLUSTAL W (1.82) Multiple Sequence Alignments

```
Sequence format is Pearson
                       296 aa
Sequence 1: Human BVR
Sequence 2: Rat_BVR
                           295 aa
                          295 aa
Sequence 3: Mouse_BVR
                           296 aa
Sequence 4: Pig_BVR
Start of Pairwise alignments Aligning...
Sequences (1:2) Aligned. Score: 82
Sequences (1:3) Aligned. Score:
Sequences (1:4) Aligned. Score:
                                98
Sequences (2:3) Aligned. Score:
                               88
Sequences (2:4) Aligned. Score:
                               83
Sequences (3:4) Aligned. Score:
Start of Multiple Alignment
There are 3 groups Aligning...
Group 1: Sequences: 2
                        Score:6353
                     2
                           Score: 6075
Group 2: Sequences:
                            Score:5825
Group 3: Sequences:
                     4
Alignment Score 9407
```

CLUSTAL W (1.82) multiple sequence alignment

Human_BVR Pig_BVR Rat_BVR Mouse_BVR	MNAEPERKFGVVVVGVGRAGSVRMRDLRNPHPSSAFLNLIGFVSRRELGSIDGVQQISLE MNAEPERKFGVVVVGVGRAGSVRMRDLRNPHPSSAFLNLIGFVSRRELGSIDGVQQISLE MDAEPKRKFGVVVVGVGRAGSVRLRDLKDPR-SAAFLNLIGFVSRRELGSLDEVRQISLE MSTEPKRKFGVVVVGVGRAGSVRIRDSKDPH-SSAFLNLIGYVSRRELGSLDNVRQISLE *.:**:********************************	60 60 59 59
Human_BVR Pig_BVR Rat_BVR Mouse_BVR	DALSSQEVEVAYICSESSSHEDYIRQFLNAGKHVLVEYPMTLSLAAAQELWELAEQKGKV DALSSQEVEVAYICSESSSHEDYIRQFLNAGKHVLVEYPMTLSLAAAQELWELAEQKGKV DALRSQEIDVAYICSESSSHEDYIRQFLQAGKHVLVEYPMTLSFAAAQELWELAAQKGRV DALRSQEVDVAYICTESSSHEDYIRQFLQAGKHVLVEYPMALSFAAAQELWELAAQKGRV *** ***:******************************	120 120 119 119
Human_BVR Pig_BVR Rat_BVR Mouse_BVR	LHEEHVELLMEEFAFLKKEVVGKDLLKGSLLFTSDPLEEDRFGFPAFSGISRLTWLVSLF LHEEHVELLMEEFAFLKKEVVGKDLLKGSLLFTAGPLEEERFGSPAFSGISRLTWLVSLF LHEEHVELLMEEFEFLRREVLGKELLKGSLRFTASPLEEERFGFPAFSGISRLTWLVSLF LHEEHIELLMEEFEFLKREVAGKELLKGSLRFTASPLEEEKFGFPAFSGISRLTWLVSLF ****:********************************	180 180 179 179
Human_BVR Pig_BVR Rat_BVR Mouse_BVR	GELSLVSATLEERKEDQYMKMTVCLETEKKSPLSWIEEKGPGLKRNRYLSFHFKSGSLEN GELSLVSATLEERKEDQYMKMTVCLETEKKSPLSWIEEKGPGLKRNRYLSFHFKSGSLEN GELSLISATLEERKEDQYMKMTVQLETQNKGLLSWIEEKGPGLKRNRYVNFQFTSGSLEE GELSLISATMENRKEDQYMKMTVQLETQNKSPLSWIEEKGPGLKRNRHISIHFKSGSLEE *****:***:**************************	240 239
Human_BVR Pig_BVR Rat_BVR Mouse_BVR	VPNVGVNKNIFLKDQNIFVQKLLGQFSEKELAAEKKRILHCLGLAEEIQKYCCSRK 296 VPNVGVNKNIFLKDQNIFVQKLLGQFSEKELAAEKKRILHCLGLAEEIQKYCCSRK 296 VPSVGVNKNIFLKDQDIFVQKLLDQVSAEDLAAEKKRIMHCLGLASDIQKLCHQKK 295 VPNVGVNKNIFLKDQDIFIQKLLGQVSAEDLAAEKKRILHCLELASDIQRLCHRKQ 295 **.**********************************	